CL

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/162,407

CRF Processing Date: 12/23/93
Edited by: _____
Verified by: MB (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

  _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

  _____

- ☐ Inserted a space between the last nucleic designator and the nucleic number for sequences:

  _____

- ☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

  _____

- ☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

  _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:

  _____

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

  _____

- ☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:

  _____

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:

  _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Other:

  _____

  _____

  _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

8/01/93

wrapped text

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia

(ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: US
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0.1
(D) SOFTWARE: Microsoft Word, Version #5.1

(vi) CURRENT APPLICATION DATA:
--> **(A) APPLICATION NUMBER: -to be assigned-**
(B) FILING DATE: December 3, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/111,758
(B) FILING DATE: August 25, 1993
--> **(C) CLASSIFICATION:**

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/106,463
(B) FILING DATE: August 12, 1993
--> **(C) CLASSIFICATION:**

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/068,394
(B) FILING DATE: May 24, 1993
--> **(C) CLASSIFICATION:**

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Malaska, Stephen L.
(B) REGISTRATION NUMBER: 32,655
(C) REFERENCE/DOCKET NUMBER: 2813-C

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 587-0430

(B) TELEFAX: (206) 233-0644
(C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GTCGACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG
GCAGAG      56

ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG
CTG   104
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
 1               5                  10                  15

CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT
TAC   152
Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
            20                  25                  30
TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA
GAG   200
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
        35                  40                  45

TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC
AAT    248
```

```
      103   Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
      104        50                  55                  60
      105
      106   CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA
-->   107   GCC   296
      108   Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
      109   65                  70                  75                  80
      110
      111   CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG
-->   112   ATG CAA   344
      113   Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
      114                 85                  90                  95
      115
      116   ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA
-->   117   TGT   392
      118   Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
      119             100                 105                 110
      120
      121   ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC
-->   122   ATC   440
      123   Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
      124           115                 120                 125
      125
      126   TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG
-->   127   CCC   488
      128   Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
      129        130                 135                 140
      130
      131   TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG
-->   132   CAG   536
      133   Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
      134   145                 150                 155                 160
      135
      136   TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA
-->   137   GCC   584
      138   Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
      139                 165                 170                 175
      140
      141   CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG
-->   142   CTC   632
      143   Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
      144             180                 185                 190
      145
      146   CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG
      147   680
      148   Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
      149           195                 200                 205
      150
      151   GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT
-->   152   GGG   728
      153   Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
```

```
      210                 215                 220

GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTGCA
TCGTTGACTC      779
Val Pro Leu Pro Ser His Pro
225                 230

AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC
AGAGCAGGAT 839

TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC
879

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 231 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein


       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
 1               5                  10                  15

Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
            20                  25                  30

Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
        35                  40                  45

Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
    50                  55                  60

Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
65                  70                  75                  80

Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
                85                  90                  95

Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
            100                 105                 110

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
        115                 120                 125

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
    130                 135                 140
```

```
205
206  Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
207  145                 150                 155                 160
208
209  Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
210                  165                 170                 175
211
212  Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
213              180                 185                 190
214
215  Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
216          195                 200                 205
217
218  Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
219      210                 215                 220
220
221  Val Pro Leu Pro Ser His Pro
222  225                 230
223
224       (2) INFORMATION FOR SEQ ID NO:3:
225
226       (i) SEQUENCE CHARACTERISTICS:
227            (A) LENGTH: 24 base pairs
228            (B) TYPE: nucleic acid
229            (C) STRANDEDNESS: single
230            (D) TOPOLOGY: linear
231
232      (iii) HYPOTHETICAL: NO
233
234      (iv) ANTI-SENSE: NO
235
236       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
237
238  TCGACTGGAA CGAGACGACC TGCT                                          24
239
240
241  (2) INFORMATION FOR SEQ ID NO:4:
242
243       (i) SEQUENCE CHARACTERISTICS:
244            (A) LENGTH: 20 base pairs
245            (B) TYPE: nucleic acid
246            (C) STRANDEDNESS: single
247            (D) TOPOLOGY: linear
248
249      (iii) HYPOTHETICAL: NO
250
251       (iv) ANTI-SENSE: NO
252
253       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
254
255  AGCAGGTCGT CTCGTTCCAG                                               20
```

```
256
257  (2) INFORMATION FOR SEQ ID NO:5:
258
259       (i) SEQUENCE CHARACTERISTICS:
260            (A) LENGTH: 988 base pairs
261            (B) TYPE: nucleic acid
262            (C) STRANDEDNESS: single
263            (D) TOPOLOGY: linear
264
265      (ii) MOLECULE TYPE: cDNA to mRNA
266
267     (iii) HYPOTHETICAL: NO
268
269      (iv) ANTI-SENSE: NO
270
271      (ix) FEATURE:
272            (A) NAME/KEY: CDS
273            (B) LOCATION: 30..734
274
275      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
276
277  CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA
278  GCC TGG    53
279                                  Met Thr Val Leu Ala Pro Ala Trp
280                                   1               5
281
282  AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG CTG AGC TCG GGA
283  CTC   101
284  Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu
285       10                  15                  20
286
287  AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC
288  GAC   149
289  Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
290   25                  30                  35                  40
291
292  TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT
293  TAC   197
294  Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
295                   45                  50                  55
296
297  CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG
298  GGC   245
299  Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
300               60                  65                  70
301
302  CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG
303  ACT   293
304  Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
305            75                  80                  85
306
```

```
      307  GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG
-->   308  GAG   341
      309  Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
      310       90                  95                  100
      311
      312  ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT
-->   313  CTT   389
      314  Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
      315  105                 110                 115                 120
      316
      317  CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC
-->   318  GAG   437
      319  Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
      320                 125                 130                 135
      321
      322  CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC
-->   323  CGG   485
      324  Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
      325               140                 145                 150
      326
      327  TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC
-->   328  CCA   533
      329  Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro
      330         155                 160                 165
      331
      332  TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG
-->   333  CCC   581
      334  Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
      335      170                 175                 180
      336
      337  CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC
      338  629
      339  Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
      340  185                 190                 195                 200
      341
      342  GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC
-->   343  CGC   677
      344  Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
      345                 205                 210                 215
      346
      347  CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG
-->   348  CTT   725
      349  Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
      350               220                 225                 230
      351
      352  GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC
      353  774
      354  Val Glu His
      355         235
      356
      357  GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG
```

--> **358 GATACTGAGG CACACAGAGG 834**

359

360 GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG

--> **361 AAGTTGGCTA GAGGCCGGTC 894**

362

363 CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA

--> **364 ATCCAGCACC 954**

365

366 GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

367

368 (2) INFORMATION FOR SEQ ID NO:6:

369

370 (i) SEQUENCE CHARACTERISTICS:
371 (A) LENGTH: 235 amino acids
372 (B) TYPE: amino acid
373 (D) TOPOLOGY: linear

374

375 (ii) MOLECULE TYPE: protein

376

377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

378

```
379 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
380   1               5                  10                  15
381
382 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
383               20                  25                  30
384
385 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
386           35                  40                  45
387
388 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
389       50                  55                  60
390
391 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
392  65                  70                  75                  80
393
394 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
395                 85                  90                  95
396
397 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
398             100                 105                 110
399
400 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
401         115                 120                 125
402
403 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
404     130                 135                 140
405
406 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
407 145                 150                 155                 160
408
```

```
409  Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
410                  165                 170                 175
411
412  Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu
413              180                 185                 190
414
415  Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
416          195                 200                 205
417
418  Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
419      210                 215                 220
420
421  Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
422  225                 230                 235
423
424  (2) INFORMATION FOR SEQ ID NO:7:
425
426       (i) SEQUENCE CHARACTERISTICS:
427            (A) LENGTH: 71 base pairs
428            (B) TYPE: nucleic acid
429            (C) STRANDEDNESS: single
430            (D) TOPOLOGY: linear
431
432      (ii) MOLECULE TYPE: cDNA to mRNA
433
434     (iii) HYPOTHETICAL: NO
435
436      (iv) ANTI-SENSE: NO
437
438
439
440
441      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
442
443  AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA
444  TGACAAGACA CCTGACTGTT  60
445
446  ACTTCAGCCA C                                                    71
447
448  (2) INFORMATION FOR SEQ ID NO:8:
449
450       (i) SEQUENCE CHARACTERISTICS:
451            (A) LENGTH: 37 base pairs
452            (B) TYPE: nucleic acid
453            (C) STRANDEDNESS: single
454            (D) TOPOLOGY: linear
455
456      (ii) MOLECULE TYPE: cDNA to mRNA
457
458     (iii) HYPOTHETICAL: NO
459
```

460 (iv) ANTI-SENSE: NO
461
462
463
464
465 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
466
467 ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG
468 37
469
470
471

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:11:06

INPUT SET: S1194.raw

Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: -to be assigned-
33	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
38	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
43	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
58	Entered (879) and Calc. Seq. Length (68) differ	(A) LENGTH: 879 base pairs
85	# of Sequences for line conflicts w/ running total	GCAGAG 56
88	# of Sequences for line conflicts w/ running total	CTG 104
93	# of Sequences for line conflicts w/ running total	TAC 152
97	# of Sequences for line conflicts w/ running total	GAG 200
102	# of Sequences for line conflicts w/ running total	AAT 248
107	# of Sequences for line conflicts w/ running total	GCC 296
112	# of Sequences for line conflicts w/ running total	ATG CAA 344
117	# of Sequences for line conflicts w/ running total	TGT 392
122	# of Sequences for line conflicts w/ running total	ATC 440
127	# of Sequences for line conflicts w/ running total	CCC 488
132	# of Sequences for line conflicts w/ running total	CAG 536
137	# of Sequences for line conflicts w/ running total	GCC 584
142	# of Sequences for line conflicts w/ running total	CTC 632
152	# of Sequences for line conflicts w/ running total	GGG 728
157	# of Sequences for line conflicts w/ running total	TCGTTGACTC 779
162	# of Sequences for line conflicts w/ running total	AGAGCAGGAT 839
260	Entered (988) and Calc. Seq. Length (129) differ	(A) LENGTH: 988 base pairs
278	# of Sequences for line conflicts w/ running total	GCC TGG 53
283	# of Sequences for line conflicts w/ running total	CTC 101
288	# of Sequences for line conflicts w/ running total	GAC 149
293	# of Sequences for line conflicts w/ running total	TAC 197
298	# of Sequences for line conflicts w/ running total	GGC 245
303	# of Sequences for line conflicts w/ running total	ACT 293
308	# of Sequences for line conflicts w/ running total	GAG 341
313	# of Sequences for line conflicts w/ running total	CTT 389
318	# of Sequences for line conflicts w/ running total	GAG 437
323	# of Sequences for line conflicts w/ running total	CGG 485
328	# of Sequences for line conflicts w/ running total	CCA 533
333	# of Sequences for line conflicts w/ running total	CCC 581
343	# of Sequences for line conflicts w/ running total	CGC 677
348	# of Sequences for line conflicts w/ running total	CTT 725
358	# of Sequences for line conflicts w/ running total	GATACTGAGG CACACAGAGG 834
361	# of Sequences for line conflicts w/ running total	AAGTTGGCTA GAGGCCGGTC 894
364	# of Sequences for line conflicts w/ running total	ATCCAGCACC 954
427	Entered (71) and Calc. Seq. Length (31) differ	(A) LENGTH: 71 base pairs
444	# of Sequences for line conflicts w/ running total	TGACAAGACA CCTGACTGTT 60
451	Entered (37) and Calc. Seq. Length (0) differ	(A) LENGTH: 37 base pairs

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:11:13

INPUT SET: S1194.raw

< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:11:14

INPUT SET: S1194.raw

Line	Original Text	Corrected Text